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0322

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RAW SEQUENCE LISTING

DATE: 03/26/2002

PATENT APPLICATION: US/10/038,723

TIME: 09:43:29

Input Set : N:\Crf3\RULE60\10038723.raw

Output Set: N:\CRF3\03262002\J038723.raw

ENTERED

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1 <110> APPLICANT: Nielsen, Bjarne Roenfeldt
2     Svendsen, Allan
3     Pedersen, Henrik
4     Vind, Jesper
5     Hendriksen, Hanne Vang
6     Frandsen, Torben Peter
7 <120> TITLE OF INVENTION: Glucoamylase Variants
8 <130> FILE REFERENCE: 5636.200-US
10 <140> CURRENT APPLICATION NUMBER: 10/038,723
11 <141> CURRENT FILING DATE: 2002-01-02
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16 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PA 1998 00937
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18 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PA 1998 01667
W--> 19 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-17
20 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/093,528
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22 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/115,545
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24 <160> NUMBER OF SEQ ID NOS: 81
25 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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28 <211> LENGTH: 1605
29 <212> TYPE: DNA
30 <213> ORGANISM: Aspergillus niger
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34 <221> NAME/KEY: mat_peptide
35 <222> LOCATION: (73)...(1602)
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (1)...(1602)
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40     Met Ser Phe Arg Ser Leu Leu Ala Leu Ser Gly Leu Val Cys Thr Gly
41           -20                      -15                      -10
42     ttg gca aat gtg att tcc aag cgc gcg acc ttg gat tca tgg ttg agc      96
43     Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Leu Asp Ser Trp Leu Ser
44           -5                      1                      5
45     aac gaa gcg acc gtg gct cgt act gcc atc ctg aat aac atc ggg gcg      144
46     Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala
47           10                      15                      20

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48	gac ggt gct tgg gtg tgc ggc gcg gac tct ggc att gtc gtt gct agt	192
49	Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser	
50	25 30 35 40	
51	ccc agc acg gat aac ccg gac tac ttc tac acc tgg act cgc gac tct	240
52	Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser	
53	45 50 55	
54	ggt ctc gtc ctc aag acc ctc gtc gat ctc ttc cga aat gga gat acc	288
55	Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr	
56	60 65 70	
57	agt ctc ctc tcc acc att gag aac tac atc tcc gcc cag gca att gtc	336
58	Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val	
59	75 80 85	
60	cag ggt atc agt aac ccc tct ggt gat ctg tcc agc ggc gct ggt ctc	384
61	Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu	
62	90 95 100	
63	ggt gaa ccc aag ttc aat gtc gat gag act gcc tac act ggt tct tgg	432
64	Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp	
65	105 110 115 120	
66	gga cgg ccg cag cga gat ggt ccg gct ctg aga gca act gct atg atc	480
67	Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile	
68	125 130 135	
69	ggc ttc ggg cag tgg ctg ctt gac aat ggc tac acc agc acc gca acg	528
70	Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr	
71	140 145 150	
72	gac att gtt tgg ccc ctc gtt agg aac gac ctg tgc tat gtg gct caa	576
73	Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln	
74	155 160 165	
75	tac tgg aac cag aca gga tat gat ctc tgg gaa gaa gtc aat ggc tgc	624
76	Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser	
77	170 175 180	
78	tct ttc ttt acg att gct gtg caa cac cgc gcc ctt gtc gaa ggt agt	672
79	Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser	
80	185 190 195 200	
81	gcc ttc gcg acg gcc gtc ggc tgc tcc tgc tcc tgg tgt gat tct cag	720
82	Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln	
83	205 210 215	
84	gca ccc gaa att ctc tgc tac ctg cag tcc ttc tgg acc ggc agc ttc	768
85	Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe	
86	220 225 230	
87	att ctg gcc aac ttc gat agc agc cgt tcc ggc aag gac gca aac acc	816
88	Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr	
89	235 240 245	
90	ctc ctg gga agc atc cac acc ttt gat cct gag gcc gca tgc gac gac	864
91	Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp	
92	250 255 260	
93	tcc acc ttc cag ccc tgc tcc ccg cgc gcg ctc gcc aac cac aag gag	912
94	Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu	
95	265 270 275 280	
96	gtt gta gac tct ttc cgc tca atc tat acc ctc aac gat ggt ctc agt	960

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97      Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser
98              285                      290                      295
99      gac agc gag gct gtt gcg gtg ggt cgg tac cct gag gac acg tac tac      1008
100      Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr
101              300                      305                      310
102      aac ggc aac ccg tgg ttc ctg tgc acc ttg gct gcc gca gag cag ttg      1056
103      Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu
104              315                      320                      325
105      tac gat gct cta tac cag tgg gac aag cag ggg tcg ttg gag gtc aca      1104
106      Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr
107              330                      335                      340
108      gat gtg tcg ctg gac ttc ttc aag gca ctg tac agc gat gct gct act      1152
109      Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Ala Thr
110      345                      350                      355                      360
111      ggc acc tac tct tcg tcc agt tcg act tat agt agc att gta gat gcc      1200
112      Gly Thr Tyr Ser Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala
113              365                      370                      375
114      gtg aag act ttc gcc gat ggc ttc gtc tct att gtg gaa act cac gcc      1248
115      Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala
116              380                      385                      390
117      gca agc aac ggc tcc atg tcc gag caa tac gac aag tct gat ggc gag      1296
118      Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu
119              395                      400                      405
120      cag ctt tcc gct cgc gac ctg acc tgg tct tat gct gct ctg ctg acc      1344
121      Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr
122      410                      415                      420
123      gcc aac aac cgt cgt aac tcc gtc gtg cct gct tct tgg ggc gag acc      1392
124      Ala Asn Asn Arg Arg Asn Ser Val Val Pro Ala Ser Trp Gly Glu Thr
125      425                      430                      435                      440
126      tct gcc agc agc gtg ccc ggc acc tgt gcg gcc aca tct gcc att ggt      1440
127      Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly
128              445                      450                      455
129      acc tac agc agt gtg act gtc acc tcg tgg ccg agt atc gtg gct act      1488
130      Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr
131              460                      465                      470
132      ggc ggc acc act acg acg gct acc ccc act gga tcc ggc agc gtg acc      1536
133      Gly Gly Thr Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr
134              475                      480                      485
135      tcg acc agc aag acc acc gcg act gct agc aag acc agc acc acg acc      1584
136      Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Thr Thr
137      490                      495                      500
138      cgc tct ggt atg tca ctg tga      1605
139      Arg Ser Gly Met Ser Leu
140      505                      510
142 <210> SEQ ID NO: 2
143 <211> LENGTH: 534
144 <212> TYPE: PRT
145 <213> ORGANISM: Aspergillus niger
146 <220> FEATURE:

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Input Set : N:\Crf3\RULE60\10038723.raw

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147 <221> NAME/KEY: SIGNAL
148 <222> LOCATION: (1)...(24)
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152   Leu Ala Asn Val Ile Ser Lys Arg Ala Thr Leu Asp Ser Trp Leu Ser
153           -5                      1                      5
154   Asn Glu Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala
155   10                      15                      20
156   Asp Gly Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser
157   25                      30                      35                      40
158   Pro Ser Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
159           45                      50                      55
160   Gly Leu Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr
161           60                      65                      70
162   Ser Leu Leu Ser Thr Ile Glu Asn Tyr Ile Ser Ala Gln Ala Ile Val
163           75                      80                      85
164   Gln Gly Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu
165   90                      95                      100
166   Gly Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp
167   105                      110                      115                      120
168   Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile
169           125                      130                      135
170   Gly Phe Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr
171           140                      145                      150
172   Asp Ile Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln
173           155                      160                      165
174   Tyr Trp Asn Gln Thr Gly Tyr Asp Leu Trp Glu Glu Val Asn Gly Ser
175   170                      175                      180
176   Ser Phe Phe Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser
177   185                      190                      195                      200
178   Ala Phe Ala Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln
179           205                      210                      215
180   Ala Pro Glu Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe
181           220                      225                      230
182   Ile Leu Ala Asn Phe Asp Ser Ser Arg Ser Gly Lys Asp Ala Asn Thr
183           235                      240                      245
184   Leu Leu Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp
185   250                      255                      260
186   Ser Thr Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu
187   265                      270                      275                      280
188   Val Val Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser
189           285                      290                      295
190   Asp Ser Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr
191           300                      305                      310
192   Asn Gly Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu
193           315                      320                      325
194   Tyr Asp Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr
195   330                      335                      340

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196   Asp Val Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Ala Thr
197   345                               355                               360
198   Gly Thr Tyr Ser Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala
199                               365                               375
200   Val Lys Thr Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala
201                               380                               390
202   Ala Ser Asn Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu
203                               395                               405
204   Gln Leu Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr
205   410                               415                               420
206   Ala Asn Asn Arg Arg Asn Ser Val Val Pro Ala Ser Trp Gly Glu Thr
207   425                               430                               435                               440
208   Ser Ala Ser Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly
209                               445                               450                               455
210   Thr Tyr Ser Ser Val Thr Val Thr Ser Trp Pro Ser Ile Val Ala Thr
211                               460                               465                               470
212   Gly Gly Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr
213   475                               480                               485
214   Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Thr Thr
215   490                               495                               500
216   Arg Ser Gly Met Ser Leu
217   505                               510
219 <210> SEQ ID NO: 3
220 <211> LENGTH: 30
221 <212> TYPE: DNA
222 <213> ORGANISM: Artificial Sequence
223 <220> FEATURE:
224 <223> OTHER INFORMATION: Primer 7258
225 <400> SEQUENCE: 3
226   gaatgacttg gttgacgcgt caccagtcac                               30
228 <210> SEQ ID NO: 4
229 <211> LENGTH: 68
230 <212> TYPE: DNA
231 <213> ORGANISM: Artificial Sequence
232 <220> FEATURE:
233 <223> OTHER INFORMATION: Primer 21401
234 <400> SEQUENCE: 4
235   ggggatcatg ataggactag ccatattaat gaagggcata taccacgcct tggacctgcg   60
236   ttatagcc                               68
238 <210> SEQ ID NO: 5
239 <211> LENGTH: 25
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial Sequence
242 <220> FEATURE:
243 <223> OTHER INFORMATION: Primer 107581
244 <400> SEQUENCE: 5
245   gcaacgaagc gcccgtaggct cgtac                               25
247 <210> SEQ ID NO: 6
248 <211> LENGTH: 88

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VERIFICATION SUMMARY

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Output Set: N:\CRF3\03262002\J038723.raw

L:14 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:17 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:19 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:21 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:23 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:445 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:14
L:445 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
L:445 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:455 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:15
L:455 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
L:455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:465 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16
L:465 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:465 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:475 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17
L:475 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:475 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:485 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18
L:485 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18
L:485 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:495 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:19
L:495 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:19
L:495 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:505 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20
L:505 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
L:505 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:515 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:515 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:525 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:22
L:525 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:535 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:535 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:535 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:545 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:545 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:555 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:555 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:555 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:565 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
L:565 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26
L:565 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:575 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27
L:575 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:575 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:585 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10038723.raw

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L:585 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
L:585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:595 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29
L:595 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:29
L:595 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:605 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:30
L:605 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:30
L:605 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:615 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:615 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:615 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:625 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:32
L:625 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:32
L:625 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:635 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:33
L:635 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:33
L:635 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:654 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:35
L:654 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:35
L:654 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:682 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:38
L:682 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:38
L:682 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:701 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:40
L:701 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:40
L:701 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:711 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:41
L:711 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:41
L:711 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:847 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:56
L:847 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:56
L:847 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56
L:857 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57
L:867 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
L:877 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59
L:887 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60
L:897 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61
L:907 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
L:1007 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73
L:1026 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75
L:1036 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76
L:1055 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:78
L:1065 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79
L:1075 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80
L:1085 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81